



SEQUENCE LISTING

<110> Pausch, Mark H
Price, Laura A

<120> Potassium Channels, Nucleotide Sequences Encoding Them,
and Methods of Using Same

<130> 01142.0122

<140> 08/816,011

<141> 1997-03-11

<160> 64

<170> PatentIn Ver. 2.1

<210> 1

<211> 2441

<212> DNA

<213> Drosophila melanogaster

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<211> 618

<212> PRT

<213> Drosophila melanogaster

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Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu
35 40 45

Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu
50 55 60

Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro
65 70 75 80

Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe
85 90 95

Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser
100 105 110

Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile
115 120 125

Gly	Ile	Pro	Val	Asn	Gly	Ile	Leu	Phe	Ala	Gly	Leu	Gly	Glu	Tyr	Phe	130	135	140	
Gly	Arg	Thr	Phe	Glu	Ala	Ile	Tyr	Arg	Arg	Tyr	Lys	Lys	Tyr	Lys	Met	145	150	155	160
Ser	Thr	Asp	Met	His	Tyr	Val	Pro	Pro	Gln	Leu	Gly	Leu	Ile	Thr	Thr	165	170	175	
Val	Val	Ile	Ala	Leu	Ile	Pro	Gly	Ile	Ala	Leu	Phe	Leu	Val	Leu	Pro	180	185	190	
Cys	Val	Gly	Val	His	Leu	Leu	Arg	Glu	Leu	Gly	Leu	Ser	Ser	Ile	Ser	195	200	205	
Leu	Tyr	Tyr	Ser	Tyr	Val	Thr	Thr	Thr	Thr	Ile	Gly	Phe	Gly	Asp	Tyr	210	215	220	
Val	Pro	Thr	Phe	Gly	Ala	Asn	Gln	Pro	Lys	Glu	Phe	Gly	Gly	Trp	Phe	225	230	235	240
Val	Val	Tyr	Gln	Ile	Phe	Val	Ile	Val	Trp	Phe	Ile	Phe	Ser	Leu	Gly	245	250	255	
Tyr	Leu	Val	Met	Ile	Met	Thr	Phe	Ile	Thr	Arg	Gly	Leu	Gln	Ser	Lys	260	265	270	
Lys	Leu	Ala	Tyr	Leu	Glu	Gln	Gln	Leu	Ser	Ser	Asn	Leu	Lys	Ala	Thr	275	280	285	
Gln	Asn	Arg	Ile	Trp	Ser	Gly	Val	Thr	Lys	Asp	Val	Gly	Tyr	Leu	Arg	290	295	300	
Arg	Met	Leu	Asn	Glu	Leu	Tyr	Ile	Leu	Lys	Val	Lys	Pro	Val	Tyr	Thr	305	310	315	320
Asp	Val	Asp	Ile	Ala	Tyr	Thr	Leu	Pro	Arg	Ser	Asn	Ser	Cys	Pro	Asp	325	330	335	
Leu	Ser	Met	Tyr	Arg	Val	Glu	Pro	Ala	Pro	Ile	Pro	Ser	Arg	Lys	Arg	340	345	350	
Ala	Phe	Ser	Val	Cys	Ala	Asp	Met	Val	Gly	Ala	Gln	Arg	Glu	Ala	Gly	355	360	365	
Met	Val	His	Ala	Asn	Ser	Asp	Thr	Asp	Leu	Thr	Lys	Leu	Asp	Arg	Glu	370	375	380	

Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu
385 390 395 400

Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu
405 410 415

Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser
420 425 430

Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr
435 440 445

Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
450 455 460

Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
465 470 475 480

Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln
485 490 495

Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met
500 505 510

Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His
515 520 525

Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp
530 535 540

Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala
545 550 555 560

Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
565 570 575

Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
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<211> 1011

<212> DNA

<213> *Caenorhabditis elegans*

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gtcactacca tcggatacgg taatccagtt ccagtgacaa acattggacg gatatgggtg 180
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<211> 336

<212> PRT

<213> *Drosophila melanogaster*

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20 25 30
Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
35 40 45
Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
50 55 60
Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly
65 70 75 80
Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
85 90 95
Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His

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Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile		
115	120	125
Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val		
130	135	140
Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser		
145	150	155
Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly		
165	170	175
Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu		
180	185	190
Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe		
195	200	205
Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val		
210	215	220
Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln		
225	230	235
Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val		
245	250	255
Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser		
260	265	270
Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile		
275	280	285
Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr		
290	295	300
Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln		
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Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys		
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<213> Caenorhabditis elegans

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<211> 24
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<213> Drosophila melanogaster

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<213> Drosophila melanogaster

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<211> 24

<212> PRT

<213> Drosophila melanogaster

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<210> 11

<211> 24

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<213> Drosophila melanogaster

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Ala Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly Tyr Gly Asp
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Met Thr Pro Val Gly Phe Trp Gly
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<210> 12

<211> 24

<212> PRT

<213> Drosophila melanogaster

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Ala Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu Gly Tyr Gly Asp
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<210> 13
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<212> PRT
<213> Drosophila melanogaster

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Ala Phe Trp Trp Ala Gly Ile Thr Met Thr Thr Val Gly Tyr Gly Asp
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Ile Cys Pro Thr Thr Ala Leu Gly
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<210> 14
<211> 24
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<213> Drosophila melanogaster

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Gly Leu Trp Trp Ala Leu Val Thr Met Thr Thr Val Gly Tyr Gly Asp
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Met Ala Pro Lys Thr Tyr Ile Gly
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<210> 15
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<213> Drosophila melanogaster

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Ala Leu Tyr Phe Thr Met Thr Cys Met Thr Ser Val Gly Phe Gly Asn
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<210> 16
<211> 24
<212> PRT
<213> Drosophila melanogaster

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1 5 10 15

Val Tyr Cys Glu Thr Val Leu Gly
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<210> 17

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<213> Drosophila melanogaster

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Ser Leu Tyr Thr Ser Tyr Val Thr Thr Thr Thr Ile Gly Phe Gly Asp
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Tyr Val Pro Thr Phe Gly Ala Asn
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<210> 18

<211> 24

<212> PRT

<213> Drosophila melanogaster

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Ile Ser Pro Thr Thr Phe Ala Gly
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<210> 19

<211> 24

<212> PRT

<213> Drosophila melanogaster

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<212> PRT

<213> Drosophila melanogaster

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<212> PRT

<213> Drosophila melanogaster

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<213> Drosophila melanogaster

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<211> 30

<212> DNA

<213> Drosophila melanogaster

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<210> 24

<211> 27

<212> DNA

<213> Drosophila melanogaster

<400> 24

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<210> 25
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<400> 29
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<400> 30

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<213> Drosophila melanogaster

<400> 31

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<210> 32

<211> 24

<212> DNA

<213> Drosophila melanogaster

<400> 32

aaaaagctta aaatgcctgg cgga

24

<210> 33

<211> 24

<212> DNA

<213> Drosophila melanogaster

<400> 33

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24

<210> 34

<211> 27

<212> DNA

<213> Drosophila melanogaster

<400> 34

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<210> 35

<211> 25

<212> DNA

<213> Drosophila melanogaster

<400> 35

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25

<210> 36

<211> 1388

<212> DNA

<213> *Caenorhabditis elegans*

<400> 36

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cccgttgtaa ttgagcactt cgtggacaag ccaagtatct tataaatatt tatagcatta 1320
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<210> 37

<211> 481

<212> PRT

<213> *Drosophila melanogaster*

<400> 37

Met Ser Pro Asn Arg Trp Ile Leu Leu Leu Ile Phe Tyr Ile Ser Tyr
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Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu

35					40					45						
Tyr	Leu	Leu	Glu	Glu	Leu	Gly	Asp	Lys	Asn	Thr	Thr	Thr	Gln	Asp	Glu	
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Ile	Leu	Gln	Arg	Ile	Ser	Asp	Tyr	Cys	Asp	Lys	Pro	Val	Thr	Leu	Pro	
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Pro	Thr	Tyr	Asp	Asp	Thr	Pro	Tyr	Thr	Trp	Thr	Phe	Tyr	His	Ala	Phe	
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Phe	Phe	Ala	Phe	Thr	Val	Cys	Ser	Thr	Val	Gly	Tyr	Gly	Asn	Ile	Ser	
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Pro	Thr	Thr	Phe	Ala	Gly	Arg	Met	Ile	Met	Ile	Ala	Tyr	Ser	Val	Ile	
115					120					125						
Gly	Ile	Pro	Val	Asn	Gly	Ile	Leu	Phe	Ala	Gly	Leu	Gly	Glu	Tyr	Phe	
130					135					140						
Gly	Arg	Thr	Phe	Glu	Ala	Ile	Tyr	Arg	Arg	Tyr	Lys	Lys	Tyr	Lys	Met	
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165					170					175						
Val	Val	Ile	Ala	Leu	Ile	Pro	Gly	Ile	Ala	Leu	Phe	Leu	Val	Leu	Pro	
180					185					190						
Cys	Val	Gly	Val	His	Leu	Leu	Arg	Glu	Leu	Gly	Leu	Ser	Ser	Ile	Ser	
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Leu	Tyr	Tyr	Ser	Tyr	Val	Thr	Ile	Thr	Thr	Ile	Gly	Phe	Gly	Asp	Tyr	
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Val	Pro	Thr	Phe	Gly	Ala	Asn	Gln	Pro	Lys	Glu	Phe	Gly	Gly	Trp	Phe	
225					230					235					240	
Val	Val	Tyr	Gln	Ile	Phe	Val	Ile	Val	Trp	Phe	Ile	Phe	Ser	Leu	Gly	
245					250					255						
Tyr	Leu	Val	Met	Ile	Met	Thr	Phe	Ile	Thr	Arg	Gly	Leu	Gln	Ser	Lys	
260					265					270						
Lys	Leu	Ala	Tyr	Leu	Glu	Gln	Gln	Leu	Ser	Ser	Asn	Leu	Lys	Ala	Thr	
275					280					285						
Gln	Asn	Arg	Ile	Trp	Ser	Gly	Val	Thr	Lys	Asp	Val	Gly	Tyr	Leu	Arg	

290		295		300
Arg Met Leu Asn Glu	Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr			
305	310	315		320
Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp				
	325	330		335
Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg				
	340	345		350
Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly				
	355	360		365
Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu				
	370	375		380
Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu				
	385	390	395	400
Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu				
	405	410		415
Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser				
	420	425		430
Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr				
	435	440		445
Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu				
	450	455		460
Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu				
	465	470	475	480

Trp

<210> 38
 <211> 337
 <212> PRT
 <213> Caenorhabditis elegans

<400> 38
 Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser
 1 5 10 15

Asn	Glu	Val	Lys	Lys	Asn	Ala	Ala	Thr	Glu	Thr	Trp	Thr	Phe	Ser	Ser			
			20						25					30				
Ser	Ile	Phe	Phe	Ala	Val	Thr	Val	Val	Thr	Thr	Ile	Gly	Tyr	Gly	Asn			
		35					40					45						
Pro	Val	Pro	Val	Thr	Asn	Ile	Gly	Arg	Ile	Trp	Cys	Ile	Leu	Phe	Ser			
	50					55					60							
Leu	Leu	Gly	Ile	Pro	Leu	Thr	Leu	Val	Thr	Ile	Ala	Cys	Leu	Ala	Gly			
	65				70					75					80			
Lys	Phe	Leu	Ser	Glu	His	Leu	Val	Trp	Leu	Tyr	Gly	Asn	Tyr	Leu	Lys			
				85					90					95				
Leu	Lys	Tyr	Leu	Ile	Leu	Ser	Arg	His	Arg	Lys	Glu	Arg	Arg	Glu	His			
			100					105						110				
Val	Cys	Glu	His	Cys	His	Ser	His	Gly	Met	Gly	His	Asp	Met	Asn	Ile			
	115						120					125						
Glu	Glu	Lys	Arg	Ile	Pro	Ala	Phe	Leu	Val	Leu	Ala	Ile	Leu	Ile	Val			
	130					135					140							
Tyr	Thr	Ala	Phe	Gly	Gly	Val	Leu	Met	Ser	Lys	Leu	Glu	Pro	Trp	Ser			
	145				150					155					160			
Phe	Phe	Thr	Ser	Phe	Tyr	Trp	Ser	Phe	Ile	Thr	Met	Thr	Thr	Val	Gly			
				165				170						175				
Phe	Gly	Asp	Leu	Met	Pro	Arg	Arg	Asp	Gly	Tyr	Met	Tyr	Ile	Ile	Leu			
			180					185					190					
Leu	Tyr	Ile	Ile	Leu	Gly	Lys	Phe	Ser	Met	Lys	Lys	Lys	Gln	Lys	Phe			
	195						200						205					
Lys	Ile	Phe	Leu	Gly	Leu	Ala	Ile	Thr	Thr	Met	Cys	Ile	Asp	Leu	Val			
	210					215					220							
Gly	Val	Gln	Tyr	Ile	Arg	Lys	Ile	His	Tyr	Phe	Gly	Arg	Lys	Ile	Gln			
	225				230					235					240			
Asp	Ala	Arg	Ser	Ala	Leu	Ala	Val	Val	Gly	Gly	Lys	Val	Val	Leu	Val			
				245					250					255				
Ser	Glu	Leu	Tyr	Ala	Asn	Leu	Met	Gln	Lys	Arg	Ala	Arg	Asn	Met	Ser			
			260					265					270					

Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile
275 280 285

Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
290 295 300

Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln
305 310 315 320

Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys
325 330 335

Xaa

<210> 39
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
primer based on human potassium channels

<400> 39
tnggatwygg wgaywy

16

<210> 40
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
sequence based on human potassium ion channels

<400> 40
rtcwccrwah ccdydgdt

18

<210> 41
<211> 28
<212> DNA
<213> Homo sapiens

<400> 41

cgcaggcaga gccacaaaga gtacacag

28

<210> 42

<211> 26

<212> DNA

<213> Homo sapiens

<400> 42

ggagatcagc taggcacat atttgg

26

<210> 43

<211> 26

<212> DNA

<213> Homo sapiens

<400> 43

atgctgcatg cctcatgctt cccagc

26

<210> 44

<211> 20

<212> DNA

<213> Homo sapiens

<400> 44

ggttatttaa agagagggt

20

<210> 45

<211> 426

<212> PRT

<213> Homo sapiens

<400> 45

Met Leu Pro Ser Ala Ser Arg Glu Arg Pro Gly Tyr Arg Ala Gly Val
1 5 10 15

Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser Lys
20 25 30

Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg Val
35 40 45

Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser Thr
50 55 60

Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val Phe
65 70 75 80

Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile Val
85 90 95

Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser Thr
100 105 110

Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala Gly
115 120 125

Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp Leu
130 135 140

Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly Phe
145 150 155 160

Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile Ile
165 170 175

Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly Val
180 185 190

Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val Glu
195 200 205

Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile Ile
210 215 220

Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala Leu
225 230 235 240

Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp Ala
245 250 255

Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr
260 265 270

Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro Val
275 280 285

Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu
290 295 300

Ser Met Ile Gly Arg Leu Val Arg Val Ile Ser Lys Lys Thr Lys Glu
305 310 315 320

Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn Val
 325 330 335

Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile Tyr
 340 345 350

Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala Glu
 355 360 365

Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr Leu
 370 375 380

Ser Val Asn His Leu Thr Ser Glu Arg Asp Val Leu Pro Pro Leu Leu
 385 390 395 400

Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Ala Pro His Cys Ala Gly
 405 410 415

Glu Glu Ile Ala Val Ile Glu Asn Ile Lys
 420 425

<210> 46

<211> 2130

<212> DNA

<213> Homo sapiens

<400> 46

ccatcctaatacgcactcact atagggctcg agcgnccgcc egggcagtaa aatgcctgcc 60
 cgtgcagctc ggagcgcgca gcccgctctc gaataagaag tgagtacaat ggcgtgtttg 120
 taaaaaaaaag cttcaagtcc gtctttttca aaaaacattt tgaatgctgc atgcctcatg 180
 cttcccagcg cctcgcggga gagaccggc tatagagcag gaggggcggc acctgacttg 240
 ctggatccta aatctgccgc tcagaactcc aaaccgaggc tctcattttc cacgaaaccc 300
 acagtgcctg cttcccgggt ggagagtgac acgaccatta atgttatgaa atggaagacg 360
 gtctccacga tattcctggg ggttgctctc tatctgatca tcggagccac cgtgttcaaa 420
 gcattggagc agcctcatga gatttcacag aggaccacca ttgtgatcca gaagcaaaca 480
 ttcatatccc aacattcctg tgtcaattcg acggagctgg atgaactcat tcagcaaata 540
 gtggcagcaa taaatgcagg gattataccg ttaggaaaca cctccaatca aatcagtcac 600
 tgggatttgg gaagttcctt cttctttgct ggcactgtta ttacaaccat aggatttggg 660
 aacatctcac cacgcacaga aggcggcaaa atattctgta tcatctatgc cttactggga 720
 attcccctct ttggttttct cttggctgga gttggagatc agctaggcac catatttggg 780
 aaaggaattg ccaaagtgga agatacgttt attaagtgga atgttagtca gaccaagatt 840
 cgcacatct caacaatcat atttatacta tttggctgtg tactctttgt ggctctgcct 900
 gcgatcatat tcaaacacat agaaggctgg agtgccctgg acgccattta ttttgtgggt 960
 atcactctaa caactattgg atttggtgac tacgttgacg gtggatccga tattgaatat 1020
 ctggacttct ataagcctgt cgtgtggttc tggatccttg tagggcttgc ttactttgct 1080
 gctgtcctga gcatgattgg gagattggtc cgagtgatat ctaaaaagac aaaagaagag 1140
 gtgggagagt tcagagcaca cgctgctgag tggacagcca acgtcacagc cgaattcaaa 1200

gaaaccagga ggcgactgag tgtggagatt tatgacaagt tccagcgggc cacctccatc 1260
aagcgggaagc tctcggcaga actggctgga aaccacaatc aggagctgac tccttgtagg 1320
aggaccctgt cagtgaacca cctgaccagc gagagggatg tcttgccctcc cttactgaag 1380
actgagagta tctatctgaa tggtttggcg ccacactgtg ctggtgaaga gattgctgtg 1440
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ttctctatgc tctttatgac tgttgctggt agcatttttt aaattgtgca tgagctcaaa 1560
gggggaacaa aatagataca cccatcatgg tcatctatca tcaagagaat ttggaattct 1620
gagccagcac tttctttctg atgatgcttg ttgaacggcc cactttcttt gatgagtga 1680
atgacaagca atgtctgatg cctttgtgtg ccagactgt tttcctctct ctttccctaa 1740
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gatcagttct taacttttca gggctacct aactgagcct agatatggac catttatgga 1860
tgacaacaat ttttttttgg taaatgacaa gaaattctta tgcagccttt tacctaagaa 1920
atttctgtca gtgccttata ttatgaagaa acagaacctc tctagctaata gtgtgggttc 1980
tccttccctg cccccacccc taggctcacc tctgcagtct tttaccccag ttctccatt 2040
tgaataccat accttgntgg aaacagngtg taaaatgact gaagtgatga tgccgaagat 2100
gaaatagatg ncaaattagn tggacattga 2130

<210> 47
<211> 27
<212> DNA
<213> Homo sapiens

<400> 47
aaaagatcta aaatgcttcc cagcgcc

27

<210> 48
<211> 27
<212> DNA
<213> Homo sapiens

<400> 48
aaagtcgacc tatttgatgt tctcaat

27

<210> 49
<211> 27
<212> DNA
<213> Homo sapiens

<400> 49
aaaaagctta aaatgcttcc cagcgcc

27

<210> 50
<211> 27
<212> DNA

<213> Homo sapiens

<400> 50

aaatctagac tatttgatgt tctcaat

27

<210> 51

<211> 534

<212> DNA

<213> Homo sapiens

<400> 51

aacaaaaacc ttttttgttt tgaatggcct agagagggtg agggatcccc tgacgaacag 60
gagcagagcc agctagaacc tgggcctggc cagttcaagg ccaccagagg gcagccttct 120
gcggaaggca gtattggggg aggcaggac cccagcagac atggcactca gagctctcac 180
tgtccactga ctctctcttc tccaggttat ggccacatgg cccactatc gccaggcgga 240
aaggccttct gcatggtctt antagccctt gggctgccag cctccttagc tctcgtggcc 300
accctgcgcc attgcctgct gcctgtgctc agccgcccac gtgcctgggt agcgggtccac 360
tggcagctgt caccggccag ggctgcgctg ctcaggcag ttgactggg actgctggtg 420
gccagcagct ttgtgctgct gccagcgtg gtgctgtggg gccttcaggg cgactgcagc 480
ctgctggggg ccgtctactt ctgcttcagc tcgctcagca ccattggcct gggg 534

<210> 52

<211> 956

<212> DNA

<213> Mus musculus

<400> 52

atgatacgat ttaatacagc tcaactatagg gaatttggcc ctcgaggcca agaattcggc 60
acgaggagaa tgtgcgcacg ttggctctca tcgtgtgcac cttcacctac ctgctgggtg 120
gcgccgcggg gttcgacgca ctggagtcgg agccggagat gatcgagcgg cagcggctgg 180
agctgcggca gctggagctg cgggcgcgct acaacctcag cgaggggcgg tacgaggagc 240
tggagcgcgt cgtgctgcgc ctcaagccgc acaaggccgg cgtgcagtgg cgcttcgccg 300
gctccttcta cttcgccatc accgtcatca ccaccatcgg ctatggcat gcggcgccca 360
gcacggacgg aggcaagggt ttctgcatgt tctacgcgct gctgggcata ccgctcacac 420
tagtcatgtt ccagagcctg ggtgaacgca tcaacacctc cgtgaggtac ctgctgcacc 480
gtgccaaagag ggggctgggc atgcggcacg ccgaagtgtc catggccaac atggtgctca 540
tcggtttcgt gtcgtgcata agcacgctgt gcatcggcgc agctgccttc tcctactacg 600
agcgtggac tttcttccag gcctattact actgcttcat caccctcacc accatcggct 660
tcggcgacta tgtggcgctg cagaaggacc aggcgtgca gacgcagccg cagtatgtgg 720
cttcagcttc gtgtacatcc tcacgggctc acggtcatcg gcgcttctc aacctcgtgg 780
tgctgcgatt catgaccatg aacgccgagg acgagaagcg tgatgcggag caccgcgcc 840
tgctcacgca caacggccag gctgtcggcc tgggtggcct gagctgcctg agcggtagcc 900
tgggcgacgg cgtgcgtccc cgcgaccag tcacatgcgc tgcggccgca agctta 956

<210> 53

<211> 1055
<212> DNA
<213> Mus musculus

<400> 53

ctgaaacat gggcccgata cctgctcctg cttatggccc acctgctggc catgggcctt 60
ggggctgtgg tgcttcaggc cctggagggc cctccagctc gccacctcca ggcccaggtc 120
caggctgaac tggctagctt ccaggcagag cacagggcct gcttgccacc tgaggccctg 180
gaggagctgc taggtgcggt cctgagagca caggcccatg gagtttccag cctgggcaac 240
agctcanaga caagcaactg ggatctgccc tcagctctgc tgttactgc cagcatcctc 300
accaccaccg gttatggcca catggcccca ctctcctcag gtggaaaggc cttctgtgtg 360
gtctatgcag cccttgggct gccagcctct ctagcacttg tggctgcctt gcgccactgc 420
ttgctgcctg tgttcagtcg cccaggtgac tgggtagcca ttcgctggca gctggcacca 480
gctcaggctg ctctgctaca ggcagcagga ctgggcctcc tgggtggcctg tgtcttcatg 540
ctgctgccag cactggtgct gtgggggtgta cagggtgact ggcagcctgc tanaaccatc 600
tacttctgtt tcggctcact cagcacgac gccctaggag acttgctgcc tgcccatgga 660
cgtggcctgc acccagccat ttaccacctt gggcagtttg cacttcttgg ttacttgctc 720
ctggggctcc tggccatggt gttagcagta gagaccttct cagagctgcc tcaggctcgt 780
gccatggtga aattcttttg gccagtggtc tctagaaccg atgaagatca agatggcatc 840
ctaggccaag atgagctggc tctgagcact gtgctgcctg acgccccagt cttgggacca 900
accacccag cctgagcggg aggcaccaag gactgcttga agaacatagc angaagggtt 960
atgggaatga atatgtcatg ggataatgtt aattttaaaa attaaatggg ctgcttagca 1020
tgcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1055

<210> 54
<211> 178
<212> PRT
<213> Homo sapiens

<400> 54

Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser
1 5 10 15
Pro Asp Gln Glu Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe
20 25 30
Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly
35 40 45
Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr
50 55 60
Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly
65 70 75 80
Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu
85 90 95

Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg
100 105 110

Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala
115 120 125

Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe
130 135 140

Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser
145 150 155 160

Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly
165 170 175

Leu Gly

<210> 55

<211> 312

<212> PRT

<213> Mus musculus

<400> 55

Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg
1 5 10 15

Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala
20 25 30

Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln
35 40 45

Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser
50 55 60

Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro
65 70 75 80

His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala
85 90 95

Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr
100 105 110

Asp Gly Gly Lys Val Phe Cys Met Phe Cys Met Phe Tyr Ala Leu Leu

115		120		125
Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile				
130		135		140
Asn Thr Ser Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly				
145		150		155
Met Arg His Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe				
		165		170
Val Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr				
		180		185
Tyr Glu Arg Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr				
		195		200
Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln				
		210		215
Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser				
		225		230
Ser Arg Ala His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg				
		245		250
Phe Met Thr Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg				
		260		265
Ala Leu Leu Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser				
		275		280
Cys Leu Ser Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val				
		290		295
Thr Cys Ala Ala Ala Ala Ser Leu				
		305		310

<210> 56

<211> 304

<212> PRT

<213> Mus musculus

<400> 56

Leu Lys Pro Trp Ala Arg Tyr Leu Leu Leu Leu Met Ala His Leu Leu
1 5 10 15

Ala Met Gly Leu Gly Ala Val Val Leu Gln Ala Leu Glu Gly Pro Pro
20 25 30

Ala Arg His Leu Gln Ala Gln Val Gln Ala Glu Leu Ala Ser Phe Gln
35 40 45

Ala Glu His Arg Ala Cys Leu Pro Pro Glu Ala Leu Glu Glu Leu Leu
50 55 60

Gly Ala Val Leu Arg Ala Gln Ala His Gly Val Ser Ser Leu Gly Asn
65 70 75 80

Ser Ser Xaa Thr Ser Asn Trp Asp Leu Pro Ser Ala Leu Leu Phe Thr
85 90 95

Ala Ser Ile Leu Thr Thr Thr Gly Tyr Gly His Met Ala Pro Leu Ser
100 105 110

Ser Gly Gly Lys Ala Phe Cys Val Val Tyr Ala Ala Leu Gly Leu Pro
115 120 125

Ala Ser Leu Ala Leu Val Ala Ala Leu Arg His Cys Leu Leu Pro Val
130 135 140

Phe Ser Arg Pro Gly Asp Trp Val Ala Ile Arg Trp Gln Leu Ala Pro
145 150 155 160

Ala Gln Ala Ala Leu Leu Gln Ala Ala Gly Leu Gly Leu Leu Val Ala
165 170 175

Cys Val Phe Met Leu Leu Pro Ala Leu Val Leu Trp Gly Val Gln Gly
180 185 190

Asp Trp Gln Pro Ala Xaa Thr Ile Tyr Phe Cys Phe Gly Ser Leu Ser
195 200 205

Thr Ile Gly Leu Gly Asp Leu Leu Pro Ala His Gly Arg Gly Leu His
210 215 220

Pro Ala Ile Tyr His Leu Gly Gln Phe Ala Leu Leu Gly Tyr Leu Leu
225 230 235 240

Leu Gly Leu Leu Ala Met Leu Leu Ala Val Glu Thr Phe Ser Glu Leu
245 250 255

Pro Gln Val Arg Ala Met Val Lys Phe Phe Gly Pro Ser Gly Ser Arg
260 265 270

Thr Asp Glu Asp Gln Asp Gly Ile Leu Gly Gln Asp Glu Leu Ala Leu
275 280 285

Ser Thr Val Leu Pro Asp Ala Pro Val Leu Gly Pro Thr Thr Pro Ala
290 295 300

<210> 57
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (1)..(9)
<223> X at positions 1, 4, and 5 is T or S; X at
position 6 is I or V; X at positions 2, 3, and 8
is Y, F, V, I, M, or L

<220>
<223> Description of Artificial Sequence: pore-forming
region of potassium channel

<400> 57
Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly
1 5

<210> 58
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (1)
<223> X at position 1 is Y or F; X at position 2 is A,
S, or G; X at positions 3, 4, 6, and 8 are M, I,
V, L, F, or Y.

<220>
<223> Description of Artificial Sequence: potassium ion
channel sequence

<400> 58

Xaa Xaa Xaa Xaa Gly Xaa Pro Xaa
1 5

<210> 59

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: potassium ion
channel sequence

<400> 59

Tyr Ala Leu Leu Gly Ile Pro
1 5

<210> 60

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> VARIANT

<222> (6)

<223> X at position 6 is M, I, V, L, F, or Y.

<220>

<223> Description of Artificial Sequence: potassium ion
channel sequence

<400> 60

Tyr Ala Leu Leu Gly Xaa Pro
1 5

<210> 61

<211> 178

<212> PRT

<213> Homo sapiens

<400> 61

Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser
1 5 10 15

Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe
20 25 30

Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly
35 40 45

Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr
50 55 60

Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly
65 70 75 80

Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu
85 90 95

Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg
100 105 110

Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala
115 120 125

Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe
130 135 140

Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser
145 150 155 160

Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly
165 170 175

Leu Glu

<210> 62

<211> 309

<212> PRT

<213> Mus musculus

<400> 62

Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg
1 5 10 15

Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala
20 25 30

Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln
35 40 45

Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser

50					55					60						
Glu	Gly	Gly	Tyr	Glu	Glu	Leu	Glu	Arg	Val	Val	Leu	Arg	Leu	Lys	Pro	
65					70					75					80	
His	Lys	Ala	Gly	Val	Gln	Trp	Arg	Phe	Ala	Gly	Ser	Phe	Tyr	Phe	Ala	
				85					90					95		
Ile	Thr	Val	Ile	Thr	Thr	Ile	Gly	Tyr	Gly	His	Ala	Ala	Pro	Ser	Thr	
			100					105					110			
Asp	Gly	Gly	Lys	Val	Phe	Cys	Met	Phe	Tyr	Ala	Leu	Leu	Gly	Ile	Pro	
		115					120					125				
Leu	Thr	Leu	Val	Met	Phe	Gln	Ser	Leu	Gly	Glu	Arg	Ile	Asn	Thr	Ser	
						135					140					
Val	Arg	Tyr	Leu	Leu	His	Arg	Ala	Lys	Arg	Gly	Leu	Gly	Met	Arg	His	
145					150					155					160	
Ala	Glu	Val	Ser	Met	Ala	Asn	Met	Val	Leu	Ile	Gly	Phe	Val	Ser	Cys	
				165					170					175		
Ile	Ser	Thr	Leu	Cys	Ile	Gly	Ala	Ala	Ala	Phe	Ser	Tyr	Tyr	Glu	Arg	
			180					185						190		
Trp	Thr	Phe	Phe	Gln	Ala	Tyr	Tyr	Tyr	Cys	Phe	Ile	Thr	Leu	Thr	Thr	
		195					200						205			
Ile	Gly	Phe	Gly	Asp	Tyr	Val	Ala	Leu	Gln	Lys	Asp	Gln	Ala	Leu	Gln	
	210					215					220					
Thr	Gln	Pro	Gln	Tyr	Val	Ala	Ser	Ala	Ser	Cys	Thr	Ser	Ser	Arg	Ala	
225					230					235					240	
His	Gly	His	Arg	Arg	Phe	Leu	Asn	Leu	Val	Val	Leu	Arg	Phe	Met	Thr	
				245					250					255		
Met	Asn	Ala	Glu	Asp	Glu	Lys	Arg	Asp	Ala	Glu	His	Arg	Ala	Leu	Leu	
		260					265						270			
Thr	His	Asn	Gly	Gln	Ala	Val	Gly	Leu	Gly	Gly	Leu	Ser	Cys	Leu	Ser	
		275					280					285				
Gly	Ser	Leu	Gly	Asp	Gly	Val	Arg	Pro	Arg	Asp	Pro	Val	Thr	Cys	Ala	
	290					295					300					
Ala	Ala	Ala	Ser	Leu												

305

<210> 63

<211> 434

<212> PRT

<213> Caenorhabditis elegans

<400> 63

Met Val Ile Ile Asn Arg Ser Asn Thr Tyr Ala Val Glu Gln Glu Ala
1 5 10 15

Phe Pro Arg Asp Lys Tyr Asn Ile Val Tyr Trp Leu Val Ile Leu Val
20 25 30

Gly Phe Gly Val Leu Leu Pro Trp Asn Met Phe Ile Thr Ile Ala Pro
35 40 45

Glu Tyr Tyr Val Asn Tyr Trp Phe Lys Pro Asp Gly Val Glu Thr Trp
50 55 60

Tyr Ser Lys Glu Phe Met Gly Ser Leu Thr Ile Gly Ser Gln Leu Pro
65 70 75 80

Asn Ala Ser Ile Asn Val Phe Asn Leu Phe Leu Ile Ile Ala Gly Pro
85 90 95

Leu Ile Tyr Arg Val Phe Ala Pro Val Cys Phe Asn Ile Val Asn Leu
100 105 110

Thr Ile Ile Leu Ile Leu Val Ile Val Leu Glu Pro Thr Glu Asp Ser
115 120 125

Met Ser Trp Phe Phe Trp Val Thr Leu Gly Met Ala Thr Ser Ile Asn
130 135 140

Phe Ser Asn Gly Leu Tyr Glu Asn Ser Val Tyr Gly Val Gly Gly Asp
145 150 155 160

Phe Pro His Thr Tyr Ile Gly Ala Leu Leu Ile Gly Asn Asn Ile Cys
165 170 175

Gly Leu Leu Ile Thr Val Val Lys Ile Gly Val Thr Tyr Phe Leu Asn
180 185 190

Asp Glu Pro Lys Leu Val Ala Ile Val Tyr Phe Gly Ile Ser Leu Val
195 200 205

Ile Leu Leu Val Cys Ala Ile Ala Leu Phe Phe Ile Thr Lys Gln Asp
210 215 220

Phe Tyr His Tyr His His Gln Lys Gly Met Glu Ile Arg Glu Lys Ala
225 230 235 240

Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu Trp Thr Thr Phe Thr Asn
245 250 255

Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu
260 265 270

Thr Ile Phe Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Gly
275 280 285

Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile Tyr Thr Leu Leu
290 295 300

Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ala Ile Gly Ser Ile Val
305 310 315 320

Ala Ser Lys Ile His Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile
325 330 335

Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Phe Cys Asn Tyr Arg
340 345 350

Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Asp Ile Phe
355 360 365

Val Ile Gly Gly Ile Ala Met Ser Phe Ser His Gly Tyr Leu Ser Ala
370 375 380

Leu Ala Met Gly Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg
385 390 395 400

Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Leu Thr
405 410 415

Gly Gly Leu Trp Pro Val Val Ile Glu His Phe Val Asp Lys Pro Ser
420 425 430

Ile Leu

<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: potassium ion
channel sequence

<220>

<221> VARIANT

<222> ()..)

<223> X at position 1 is Y or F; X at position 2 is A, S,
or G; X at positions 3, 4, and 6 are M, I, V, L,
F, or Y.

<400> 64

Xaa Xaa Xaa Xaa Gly Xaa Pro
1 5